

Docket No.: PF-0319-2 DIV  
Inventors: Bandman et al.  
Title: HUMAN PROTEIN PHOSPHATASE  
Serial No.: To Be Assigned

9	18	27	36	45	54
5' NNA TAT TGT ACC TAT CAG GCG TCA GCT CTC AAT CTA GAT CCC TCC CTG GCC TCG					
GAC TTA TIG CAA AAC ATG GGT GCT TTT TIG GAT AAA CCC AAA ACT GAA AAA CAT	63	72	81	90	99
M G A F L D K P K T E K H					
AAT GCT CAT GGT GCT GGG AAT GGT TTA CGT TAT GGC CTG AGC AGC ATG CAA GGA	117	126	135	144	153
N A H G A G N G L R Y G L S S M Q G					
TGG AGA GTG GAA ATG GAA GAT GCA CAC ACA GCT GTT GTA GGT ATT CCT CAC GGC	171	180	189	198	207
W R V E M E D A H T A V V G I P H G					
TIG GAA GAC TGG TCA TTT GCA GTT TAT GAT GGT CAT GCT GGA TCC CGA GTG	225	234	243	252	261
L E D W S F F A V D G H A G S R V					
GCA AAT TAC TGC TCA ACA CAT TTA TTA GAA CAC ATC ACT ACT AAC GAA GAC TTT	279	288	297	306	315
A N Y C S T H L L E H I T N E D F					
AGG GCA GCT GGA AAA TCA GGA TCT GCT CTT GAG CTT TCA GTG GAA AAT GTT AAG	333	342	351	360	369
R A A G K S G S A L E S V E N V K					

FIGURE 1A

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387	AAT	GGT	ATC	AGA	ACT	GGA	TTC	TTC	AAA	ATT	GAT	GAA	TAC	ATG	CGT	AAC	TTT	TCA
N	G	I	R	T	G	F	L	K	I	D	E	Y	M	R	N	F	S	
441	GAC	CTC	AGA	AAC	GGG	ATG	GAC	AGG	AGT	GGT	TCA	ACT	GCA	GTG	GGA	GTP	ATG	ATT
D	L	R	N	G	M	D	R	S	G	S	T	A	V	G	V	M	I	
495	TCA	CCT	AAG	CAT	ATC	TAC	TTC	ATC	AAC	TGT	GAT	TCA	CGT	GCT	GTT	CTG	TAT	
S	P	K	H	I	Y	F	I	N	C	G	D	S	R	A	V	L	Y	
549	AGG	AAT	GGA	CAA	GTC	TGC	TTC	TTC	TCT	ACC	CAG	GAT	CAC	AAA	CCT	TGC	ATA	AGG
R	N	G	Q	V	C	F	S	T	Q	D	H	K	P	C	N	P	R	
603	GAA	AAG	GAG	CGA	ATC	CAA	AAT	GCA	GGG	GGC	AGC	GTG	ATG	ATA	CAA	CGT	GTT	AAT
E	K	E	R	I	Q	N	A	G	G	S	V	M	I	Q	R	V	N	
657	GGT	TCA	TTA	GCA	GTA	TCT	CGT	GCT	CTG	GGG	GAC	TAT	GAT	TAC	AAG	TGT	GTT	AAT
G	S	L	A	V	S	R	A	L	G	D	Y	D	Y	K	C	V	D	
711	GGC	AAG	GGC	CCA	ACA	GAA	CAA	CTT	GGT	TCT	CCA	GAG	CCT	GAG	GTP	TAT	GAA	ATT
G	K	G	P	T	E	Q	L	V	S	P	E	P	E	V	Y	E	I	

FIGURE 1B

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L	R	A	E	D	F	I	L	A	C	D	G	I	W	D
V	M	S	N	E	E	L	C	E	Y	V	K	S	R	L
GAT	GAC	CTG	GAA	AAT	GTG	TGC	AAT	TGG	GTA	GTG	GAC	ACT	TGT	TCA
D	D	L	E	N	V	C	N	W	V	V	D	T	C	L
S	R	D	N	M	S	I	V	L	V	C	F	S	N	A
927	936	945	945	945	945	945	945	945	945	945	945	945	945	945
TCA	GAT	GAA	AGT	ATT	GTA	CTA	GTT	TGC	TTT	TCA	AAT	GCT	CCC	AAG
S	D	E	A	V	K	K	D	S	E	L	D	K	H	L
981	990	999	999	999	999	999	999	999	999	999	999	999	999	999
GTT	GAA	GAG	ATT	ATG	GAG	AAG	TCT	GGC	GAG	GAA	GGA	ATG	CCT	GAT
V	E	E	I	M	E	K	S	G	E	E	M	P	D	L
1035	1044	1053	1053	1053	1053	1053	1053	1053	1053	1053	1053	1053	1053	1053
GTC	ATG	CGC	ATC	TTG	TCT	GCA	GAA	AAT	ATC	CCA	AAT	TTG	CCT	GGG
V	M	R	I	L	S	A	E	N	I	P	N	L	P	G

FIGURE 1C

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1143	1152	1161	1170	1179	1188
CTT GCT GGC AAG CGT AAT GTT ATT GAA GCT GTT TAT AGT AGA CTG AAT CCA CAT	L A G K R N V I E A V Y S R L N P H				
1197	1206	1215	1224	1233	1242
AGA GAA AGT GAT GGG GCC TCC GAT GAA GCA GAG GAA AGT GGA TCA CAG GGA AAA	R E S D G A S D E A E E S G S Q G K				
1251	1260	1269	1278	1287	1296
TTC GTC GAA GCT CTC AGG CAA ATG AGA ATT AAT CAT AGG GGA AAC TAC CGA CAA	L V E A L R Q M R I N H R G N Y R Q				
1305	1314	1323	1332	1341	1350
CTT CTG GAG GAG ATG CTG ACT AGT TAC AGG CTA GCT AAA GTA GAG GGA GAA GAA	L L E M L T S Y R L A K V E G E E				
1359	1368	1377	1386	1395	1404
AGC CCT GCT GAA CCA GCT GCC ACA GCT ACT TCT TCG AAC AGT GAT GCT GGA AAC	S P A E P A A T A T S S N S D A G N				
1413	1422	1431	1440	1449	1458
CCA GTG ACA ATG CAG GAA AGC CAT ACT GAA TCA GAA AGT GGT CTT GCT GAA TTA	P V T M Q E S H T E S E S G L A E L				
1467	1476	1485	1494	1503	1512
GAC AGC TCT AAT GAA GAT GCA GGG ACA AAG ATG AGT GGT GAA AAA ATA TGA CTT	D S S N E D A G T K M S G E K I				

FIGURE 1D

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TCC	TTT	TTG	GTA	ATA	TTT	TTG	TGA	TCT	TTG	ATG	GTT	TTT	AAC	C <sub>TA</sub>	GGA	AGT	GTA	1566
ATG	TAT	GCA	TTT	ATA	TAA	CTG	TTT	TGT	TAT	TTG	AAT	CTT	GGA	AAA	CTA	GTT	TTA	1620
TTA	TAT	TCA	GAT	AGC	CTT	GTT	TTT	TAA	AAA	GGC	C <sub>TT</sub>	TGC	ATA	CAC	CTT	TAT	GAG	1674
1629	1638	1647	1656	1665	1674													
1683	1692	1701	1710	1719	1728													
TTT	CAC	ATT	GTA	TGC	CAG	AAA	TTA	GGC	TAC	CAA	TTA	TGA	ATT	AAA	GTC	AGT	AGT	1782
1737	1746	1755	1764	1773	1782													
TAA	ATT	AAT	ACT	AGA	TAG	AAT	TAG	AAA	TTT	TGA	TTA	GAG	AGA	T <sub>TA</sub>	TGC	TAT	ATT	
1791	1800	1809	1818	1827	1836													
ATG	GAA	AAA	C <sub>TT</sub>	GTT	AAT	GTA	GAA	TTA	TAC	TGC	TTC	ATA	TTA	TTT	TAC	CTA	TTA	1890
1845	1854	1863	1872	1881	1890													

FIGURE 1E

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1899	1908	1917	1926	1935	1944
GTA CAC TCA TAG TTA GCT TTG TAA ATT TAT GTT TTC TTT AAT ATA ATT AGT					
1953	1962	1971	1980	1989	1998
TCT TCA AAG AAT GGC TGA TGC TGG CCT GTA ATT TTT CTT TCA AGG ATG ATA ATT					
2007	2016	2025	2034	2043	2052
TGT GTG TTG TTT GAT TTG ATT TTT TAC ATC TCT GTA GTT TTA TTT TTA GAA					
2061	2070	2079	2088	2097	2106
GTG AGA TAT TGG ATG TGT GGC TAT TTT TCC TTT CTC TGT ATT CTT TAT GAA					
2115	2124	2133	2142	2151	2160
ACA TAA CTT TTG AAA AAC CTA TGT ATT CAT ACA GCT TTG GTC TGT ATA TTC					
2169	2178	2187	2196	2205	2214
TGT ATA GCC TAA CTA CAC ACA TCA AAA TGT ATG TCA ACC AAG TGT TTA GAA TGA					
2223	2232	2241	2250	2259	2268
AAT TAT AAG TGT TTA AGT CCA AAT AAA GCA TGT GAT GTG GAA TAA TCA AAA AAA					

FIGURE 1F

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FIGURE 1G

AA 3'

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1	M G A F L D K P K T E K H N A H G A G N G L R Y G L S S M Q G W R V E M E D A H	13177
1	M G A F L D K P K T E K H N A H G A G N G L R Y G L S S M Q G W R V E M E D A H	GI 247927
1	M G A F L D K P K T E K H N A H G A G N G L R Y G L S S M Q G W R V E M E D A H	GI 452526
41	T A V V G I P H G L E D W S F F A V Y D G H A G S R V A N Y C S T H L L E H I T	13177
41	T A V V G I P H G L E D W S F F A V Y D G H A G S R V A N Y C S T H L L E H I T	GI 247927
41	T A V V G I P H G I P H G L D N W S F F A V Y D G H A G S R V A N Y C S T H L L E H I T	GI 452526
81	T N E D F R A A G K S G S A L E L S V E N V K N G I R T G F L K I D E Y M R N F	13177
81	T N E D F R A A D K S G F A L E P S V E N V K T G I R T G F L K I D E Y M R N F	GI 247927
81	T N E D F R A A D K S G S A L E P S V E S V K T G I R T G F L K I D E Y M R N F	GI 452526
121	S D L R N G M D R S G S T A V G V M I S P K H I Y F I N C G D S R A V L Y R N G	13177
121	S D L R N G M D R S G S T A V G V M I S P T H I Y F I N C G D S R A V L C R N G	GI 247927
121	S D L R N G M D R S G S T A V G V M V S P T H M Y F I N C G D S R A V L C R N G	GI 452526
161	Q V C F S T Q D H K P C N P R E K E R I Q N A G G S V M I Q R V N G S L A V S R	13177
161	Q V C F S T Q D H K P C N P M E K E R I Q N A G G S V M I Q R V N G S L A V S R	GI 247927
161	Q V C F S T Q D H K P C N P V E K E R I Q N A G G S V M I Q R V N G S L A V S R	GI 452526
201	A L G D Y D Y K C V D G K G P T E Q L V S P E P E V Y E I L R A E E D E F I L	13177
201	A L G D Y D Y K C V D G K G P T E Q L V S P E P E V Y E I L R A E E D E F V V L	GI 247927
201	A L G D Y D Y K C V D G K G P T E Q L V S P E P E V Y E I V R A E E D E F V V L	GI 452526

FIGURE 2A

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241	A C D G I W D V M S N E E L C E Y V K S R L E V S D D L E N V C N W V V D T C L	13177
241	A C D G I W D V M S N E E L C E F V N S R L E V S D D L E N V C N W V V D T C L	GI 247927
241	A C D G I W D V M S N E E L C E F V K S R L E V S D D L E N V C N W V V D T C L	GI 452526
281	H K G S R D N M S I V L V C F S N A P K V S D E A V K K D S E L D K H L E S R V	13177
281	H K G S R D N M S I V L V C F A N A P K V S D E A V K R D E L D K H L E S R V	GI 247927
281	H K G S R D N M S V V L V C F S N A P K V S E E A V K R D S E L D K H L E S R V	GI 452526
321	E E I M E K S G E E G M P D L A H V M R I L S A E N I P N L P P G G G L A G K R	13177
321	E E I M Q K S G E E G M P D L A H V M R I L S A E N I P N L P P G G G L A G K R	GI 247927
321	E E I M Q K S G E E G M P D L A H V M R I L S A E N I P N L P P G G G L A G K R	GI 452526
361	N V I E A V Y S R L N P H R E S D G A S D E A E E S G S Q G K L V E A L R Q M R	13177
361	N V I E A V Y S R L N P N K D N D G G A G D - - - - - - - - - - - - - - - - -	GI 247927
361	H V I E A V Y S R L N P H K D N D G G A G D - - - - - - - - - - - - - - - - -	GI 452526
401	I N H R G N Y R Q L L E E M L T S Y R L A K V E G E E S P A E P A A T S S N	13177
383	- - - - - - - - - L E D S L V A -	GI 247927
383	- - - - - - - - - L E D S L V A -	GI 452526
441	S D A G N P V T M Q E S H T E S E S G L A E L D S S N E D A G T K M S G E K I	13177
390	- L	GI 247927
390	- L	GI 452526

FIGURE 2B

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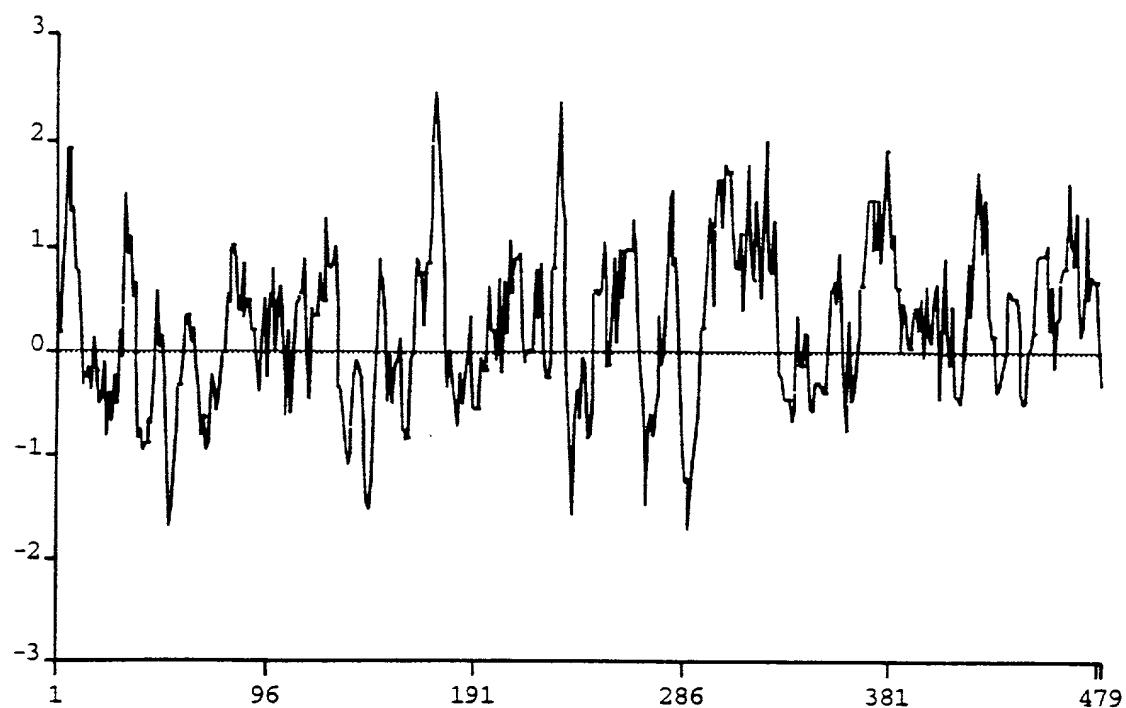


FIGURE 3A

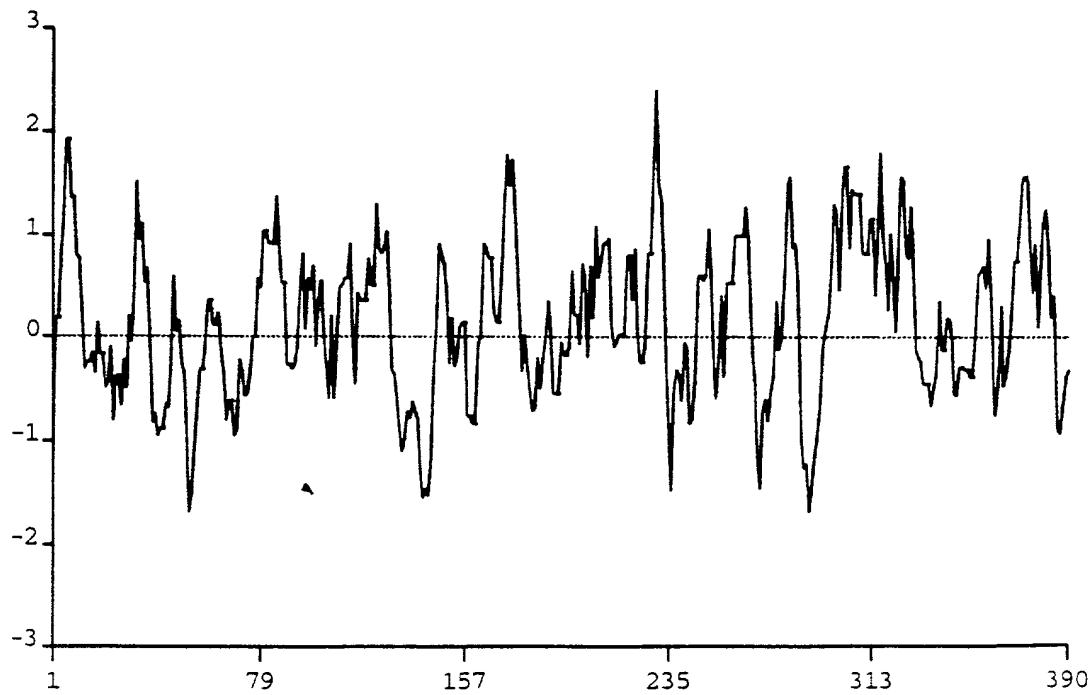


FIGURE 3B